

MPRIMIKGGVWRNTEDEILKAAVMKYGKNQWSRIASLLHRKSAKQCKARW 50
 YEWLDPSIKKTEWSREEEKLLHLAKLMPTQWRTIAPIIGRTAAQCLEHY 100
 EFLLDKAAQRDNEEETTDDPRKLKPGEIDPNPETKPARPDPIDMDEDELE 150
 MLSEARARLANTQGKKAKRKAREKQLEEARRLAALQKRRELRAAGIEIQK 200
 KRKRKRGVDYNAEIPFEKKPALGFYDTSEENYQALDADFRKLRQQDLGE 250
 LRSEKEGRDRKKDKOHLKRKKESDLPSAILQTSGVSEFTKKRSKLVLPAP 300
 QISDAELQEVVKVGQASEIARQTAEESGITNSASSTLLSEYNVTNNSVAL 350
 RTPRTPASQDRILQEAQNLMAITNVDTPKGGNTPLHESDFSGVTPQRO 400
 VVQTPNTVLSTPFRTPSNGAEGLTTPRS GTTPKPVINSTPGRTPLRDKLN 450
 NPEDGMADYSDPSYVKOMERESREHLRLGLLGLPAPKNDFEIVLPENAEK 500
 ELEEREIDDTYIEDAADVDARKQAIRDAERVKEMKRMHKAVQKDLPRPSE 550
 VNETILRPLNVEPPLTDLQKSEELIKKEMITMLHYDLLHHPYEPGKNGG 600
 KTVGFGTNNSEHITYLEHNPYEKFSKEELKKAQDVLVQEMEVVKQGM SHG 650
 ELSSEAYNQWEECYSQLYLPGQSR YTRANLASKKDRIESLEKRLEINR 700
 GHMTTEAKRAAKMEKKMKILLGGYQSRAMGLMKQLNDLWDQIEQAHLER 750
 TFEELKKHEDSAIPRRLECLKEDVQRQQEREKELQHRYADLLLEKETLKS 800

KF*

Fig. 1A

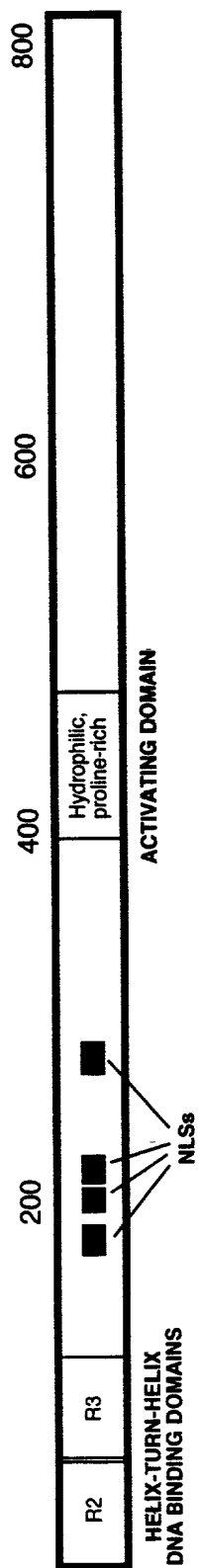


Fig. 1B

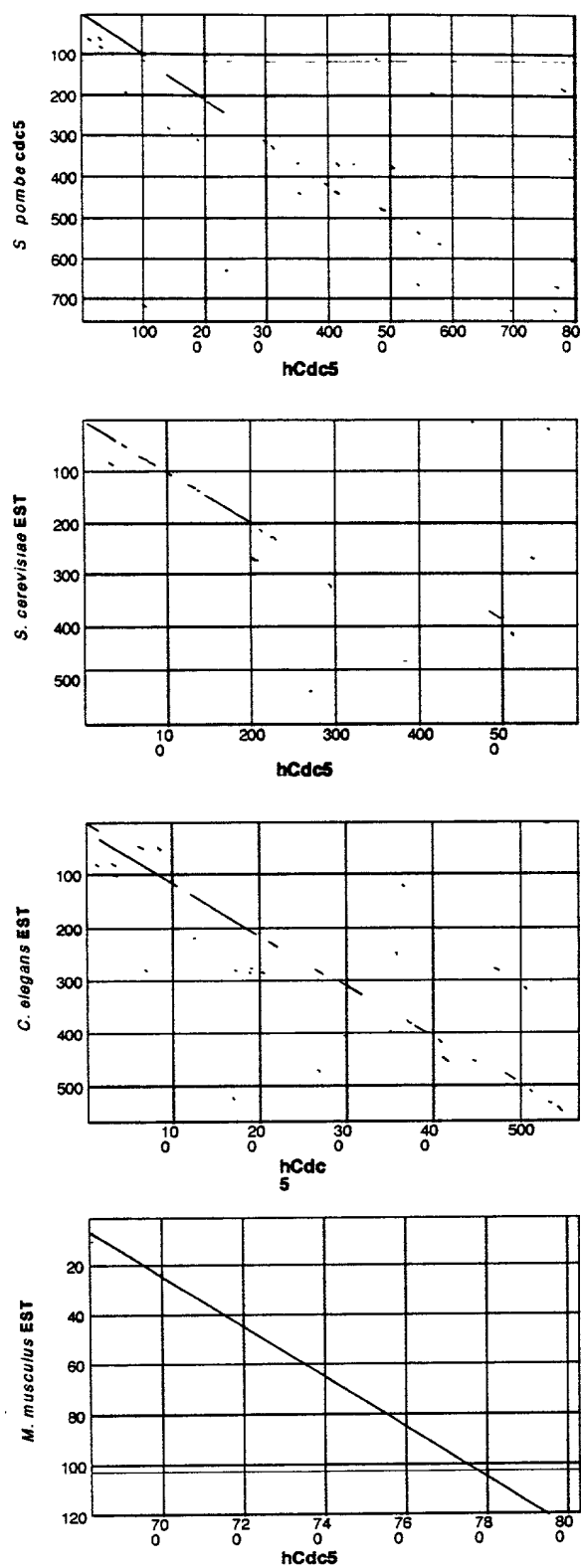


Fig. 2A

hCdc5	IKGGVWRNTEDEILKAAVMKYGKNQWSRIASLLHRKSAKQCKARWYEWLDP	(6-56)
<i>Spombe</i> cdc5	LIKGGAWKNTEDEILKAAVSKYGKNQWARISSLLVRKTPKQCKARWYEWIDP	(5-55)
b-Myb	V/K-GPWTKEEDQKVIELVKKYGTQKWTLLIAKHLKGRLGKQCRERWNNHLLNP	(88-137)
a-Myb	IK-GPWTKEEDQKVIELVQKYGPKRWSLIAKHLKGRIGKQCRERWNNHLLNP	(87-136)
c-Myb	IK-GPWTKEEDQKVIELVQKYGPKRWSVIAKHLKGRIGKQCRERWNNHLLNP	(92-141)

Fig. 2B

hCdc5	PLKGGGLNTPLHESDFSGVTPQRQVVQTPNTVLSTPFRTPSNGAEGLTPRSGLTPKPVINSTP (378-439)
<i>S. pombe</i> cdc5	SVTIEVRNQLMNREQSSLLGQESIPQGGTGYTGVT-PSHAANGS---ALAAP--Q--ATP (380-434)
b-Myb	PVK-TL--PFSPSQFLNFWNKQDTLEESPLSTPVCQKVVVTTPLHRDKTPLHQQKHAFAF (445-503)
a-Myb	ILRKKRKMVRVGHSPGSEL-RDGSUNDGGNMALKTPLKTPFSPSQFFNTCPGNEQLNIENPSF (446-508)
hCdc5	GRTPLRDKLNPREDGMADYSDPSYVKQMERESREHLRLGLLGLPAPKNDFEIVLPENAEK (440-500)
<i>S. pombe</i> cdc5	FRTPR-DTFSINAAERAGR-LASE-REN-KIRLKALRELLAKLPKPKNDYEL-ME-P-R- (435-487)
b-Myb	VTPDQKYSMDNTRHTP-TPFKNAKYGPLKPLPQTPHLEEDLKEVLRSEAGIELIIEDDIRP (504-565)
a-Myb	TSTPICGQKAL-ITTPLHKETTPKDQKENVGFRPTIIRRSILGTPRTPTPFKNALAAQEKK (509-569)

Fig. 2C

5' untranslated region:

GGCAGGAGAGGAAGTGGCGGGCTTTGAGTCCGGTGGCCCAATCGCTGTACTAGTTCTCTGAAGCTCCTCTCGGCTGCTTGC
CGAGACACCTTGGCGCCAAG

Coding region:

1 DNA BINDING DOMAIN (___)
1 atgcctcgaat ttatgatcaa gggggggccta tggaggaata ccgaggaatga aattctgaaa
61 gcagcggtaaa tgaatatatga gaaaaatcaa tggctctagga ttgcctcatt gctgcataga
121 aaatcagcaa agcagtgcaa agccagatga tatgaatggc tggatccaaq cattaagaaq
181 acagaatggt ccagagaaga agaggaaaaa ctcttgacat tggccaagtt gatcccaact
241 cagtggaaga ccattgctcc aatcattgga agaacagcgg ccagtgctt agaacacrat
301 gaattttcttc tggataaagg tgcccaaaga gacaatgaag aggaacaac agatgatcca
361 cgaaaactta aacctggaga aatagatcca aatccagaaa caaaaccagc gcggcctgat
421 ccaattgata tggatgagga tgaacttgag atgctttctg aagccagagc ccgcttggtt
2 NUCLEAR LOCALIZATION DOMAIN (....)
481 aatactcagg gaaagaaggc caagagggaaa gcaagagaga aacaattgga agaagcaaga
541 cgtcttgctg cctccaaaa aagaagagaa ctctgagcag ctggcataga aattcagaag
601 aaaagaaaaa ggaagagagg agttgattat aatgccgaaa tcccatttga aaaaaagcct
661 gcccttggtt ttatgatata ttctgaggaa aactaccaag ctcttgacgc agatttcagg
721 aaattaagac aacaggatct tgatggggag ctaagatctg aaaaagaagg aagagataga
781 aaaaaagaca aacagcattt gaaaagggaaa aaagaatctg atttaccatc agctattctt
841 caaactagtg gtgtttctga atttactaaa aagagaagca aactagtact tcctgcccct
901 cagatttcag atgcagaact ccaggaagtt gtaaaagtag gccaagcgag tgaatttga
961 cgtcaaactg ccgaggaatc tggcataaca aattctgctt ccagtacact ttgtctgag
1021 tacaatgtca ccaacaacag cgttgtctt agaacaccac gaacaccagc ttcccaggac
1081 agaattctgc aggaagccca gaacctcatg gccctcacca atgtggacac cccattgaaa
3 ACTIVATING DOMAIN (___)
1141 ggtggactta ataccctcatt gcattgagat gacttctcag gtgtaactcc acagcgacaa
1201 gttgtacaga ctccaaacac agttctctct actccattca ggactccttc taatggagct
1261 gaagggctga ctccccggag tggaaacaact cccaaaccag ttattaactc tactccgggt
1321 agaactcctc ttcgagacaa gttaaacatt aatcccagag atggaatggc agactatagt
1381 gatccctctt acgtgaagca gatggaaga gaatcccag aacatctccg tttagggttg
1441 ttgggccttc ctgcccctaa gaatgatttt gaaattgttc taccagaaaa tgccgagaag
1501 gagctggaag aacgtgaaat agatgatact tacattgaag atgctgctga tgtggatgct
1561 cgaaagcagg ccatacgaga tgcagagcgt gtaaaaggaaa tgaaacgaat gcataaagct
1621 gtccagaaa atctgccaag accatcagaa gtaaatgaaa ctattctaaag acccttaaat
1681 gtagaaccgc ctttaacaga ttacagaaa agtgaagaac taatcaaaaa agaaatgatc
1741 acaatgcttc attatgacct tctacatcac ccttatgaac catctggaaa taaaaaggc
1801 aaaactgtag ggtttggtac caataattca gagcacatta cctatctgga acataatcct
1861 tatgaaaagt tctccaaaga agagctgaaa aaggcccagg atgttttggt gcaggagatg
1921 gaagtggtta aacaaggaat gagccatgga gagctctcaa gtgaagctta taaccagggtg
1981 tgggaagaat gctacagtca agttttatat ctctctgggc agagccgcta cacacggggc
2041 aatctggcta gtaaaaagga cagaattgaa tcacttgaaa agaggctcga gataaacagg
2101 ggtcacatga cgacagaagc caagagggct gcaaagatgg aaaagaagat gaaaattttg
2161 cttgggggtt accagtctcg tgctatgggg ctcatgaaac agttgaatga cttatggggac
2221 caaattgaac aggtctcact ggagttacgc acttttgaag aactcaagaa acatgaagat
2281 tctgctatc cccggaggct agagtgtcta aaagaagacg ttcagcgaca acaagaaaga
2341 gaaaaggaac ttcaacatag atatgtgat ttgctgctgg agaaagagac tttaaagtca
2401 aaattctga

3' untranslated region:

AGTACAGTTTATCTCTGTCACAGGATTAATTAATGCGGGTTTCATCTCTAGAGGCTGAAACTG ATGTTTATCTTCATTGACA
AATTTACCCACCATCTGTGGTTTTCAGTTGTTTATTTAAATGATATCGATCTTACACATCTGTGTATAAAGACCTTAACCTCACA
GGACGGACATTTTAGAGTTTAAATTATTA AGGCTATCATCTTTTAGTAATGTCATATTGCAAACTTTTATGTTTGGCCTTTAA
TTTAAAAAGCCTAATTTTAAAGTGCTGCTGTGAGTAACCTTTGAATAAAACAAATATATAAAA

Fig. 2D

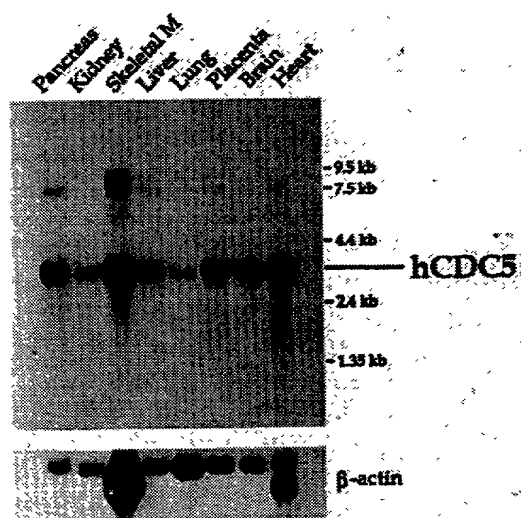


FIG. 3

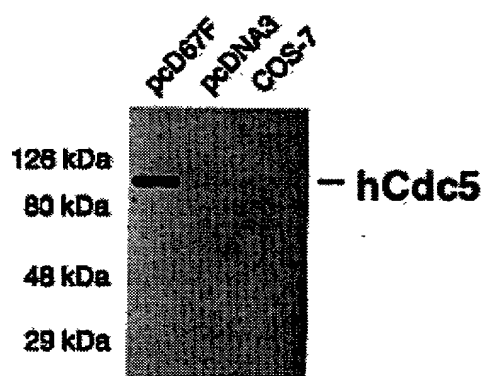


FIG. 4A

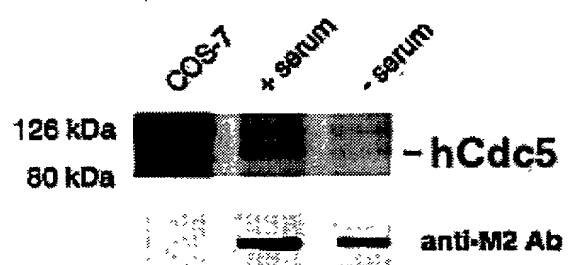


FIG. 4B

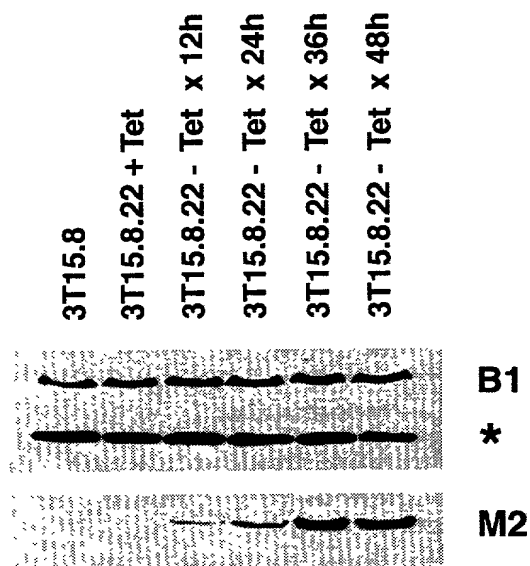


FIG. 5

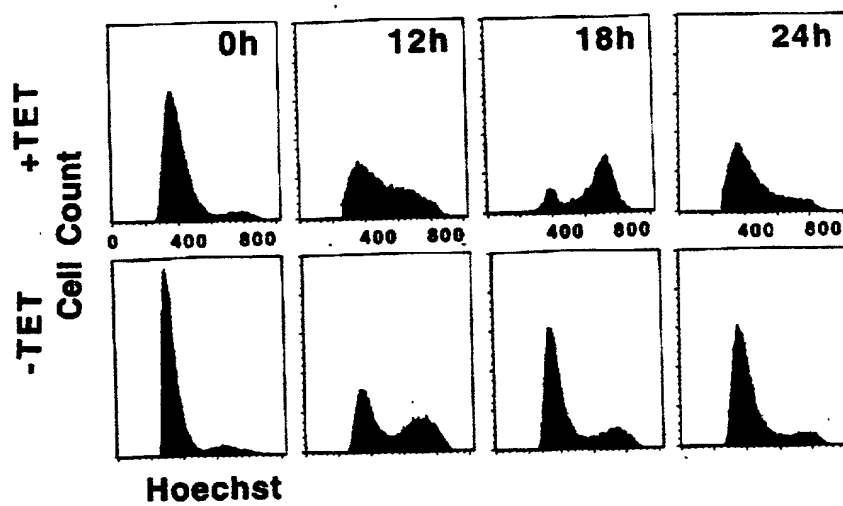


Fig. 6

00000-64025260

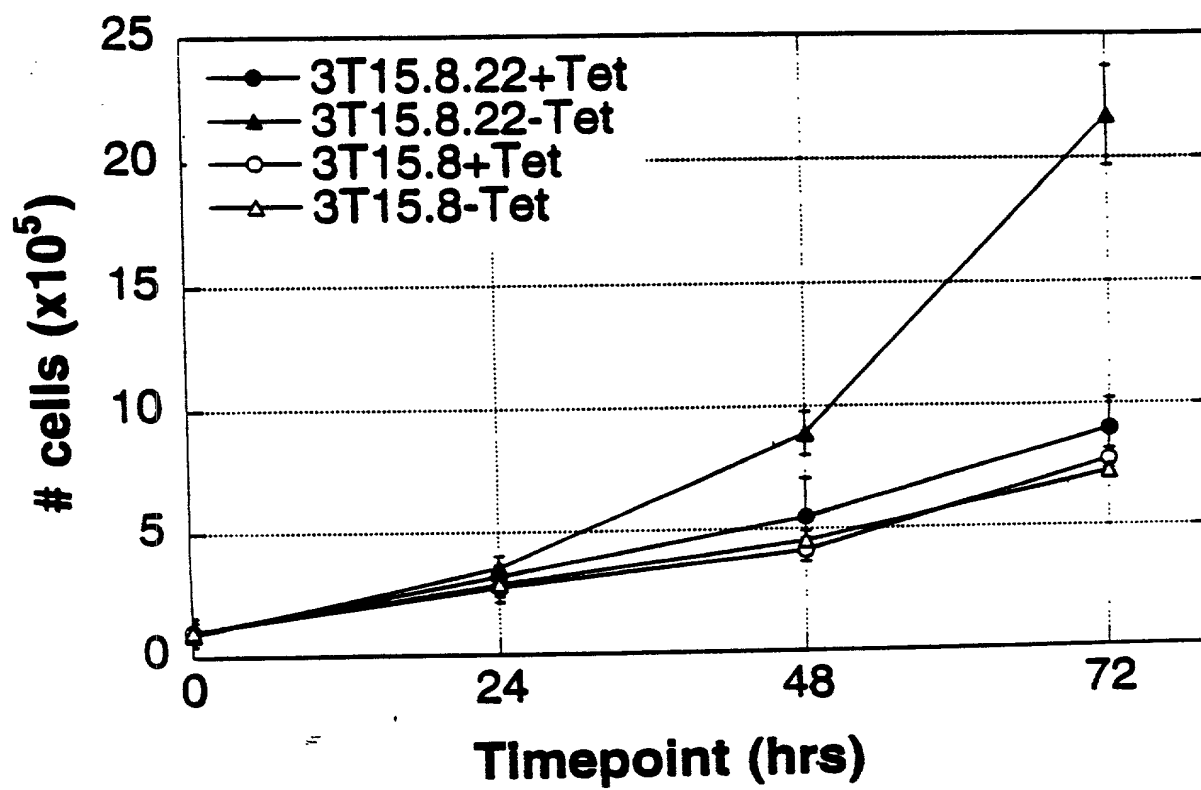


Fig. 7

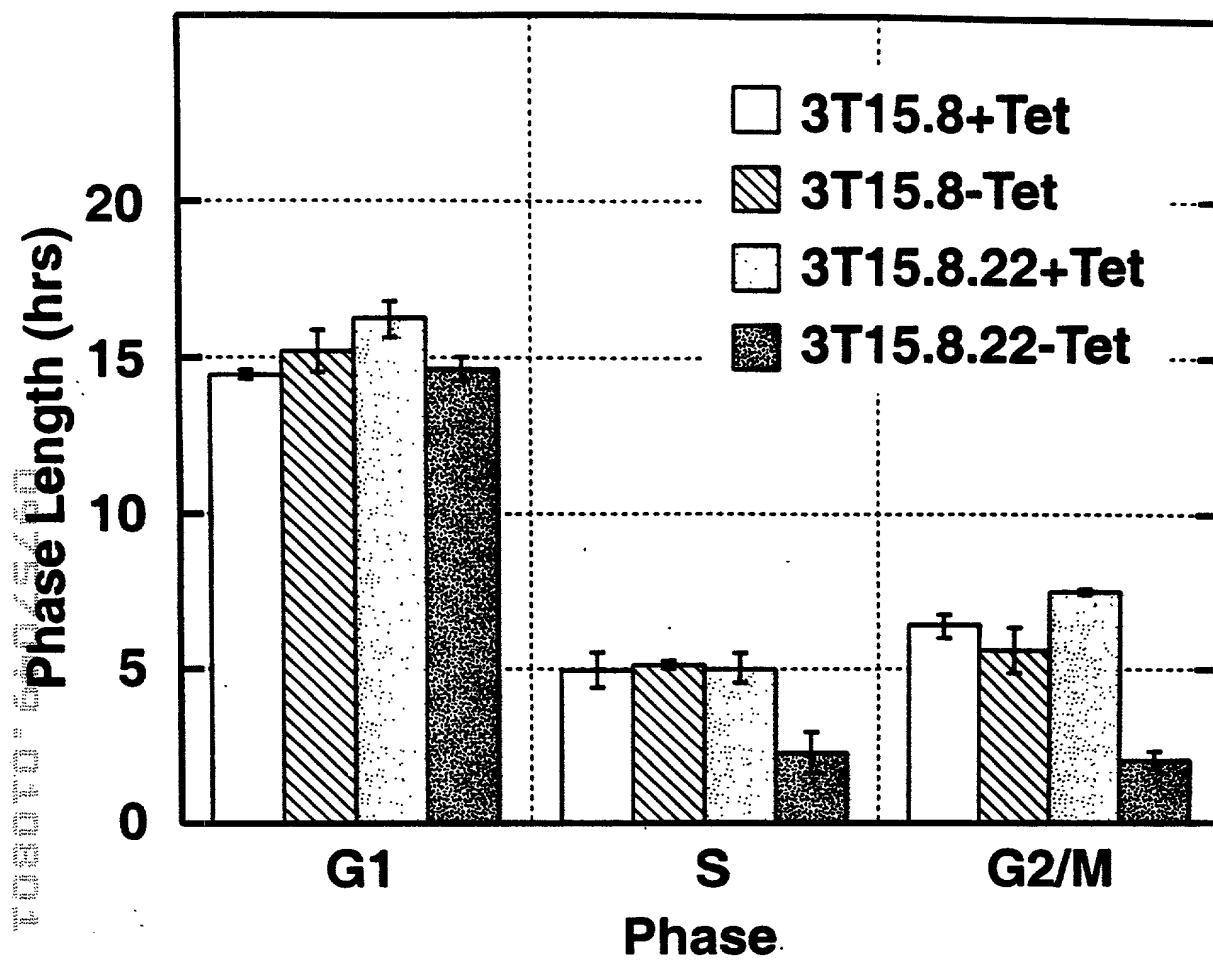


FIG. 8

20250402 09:00

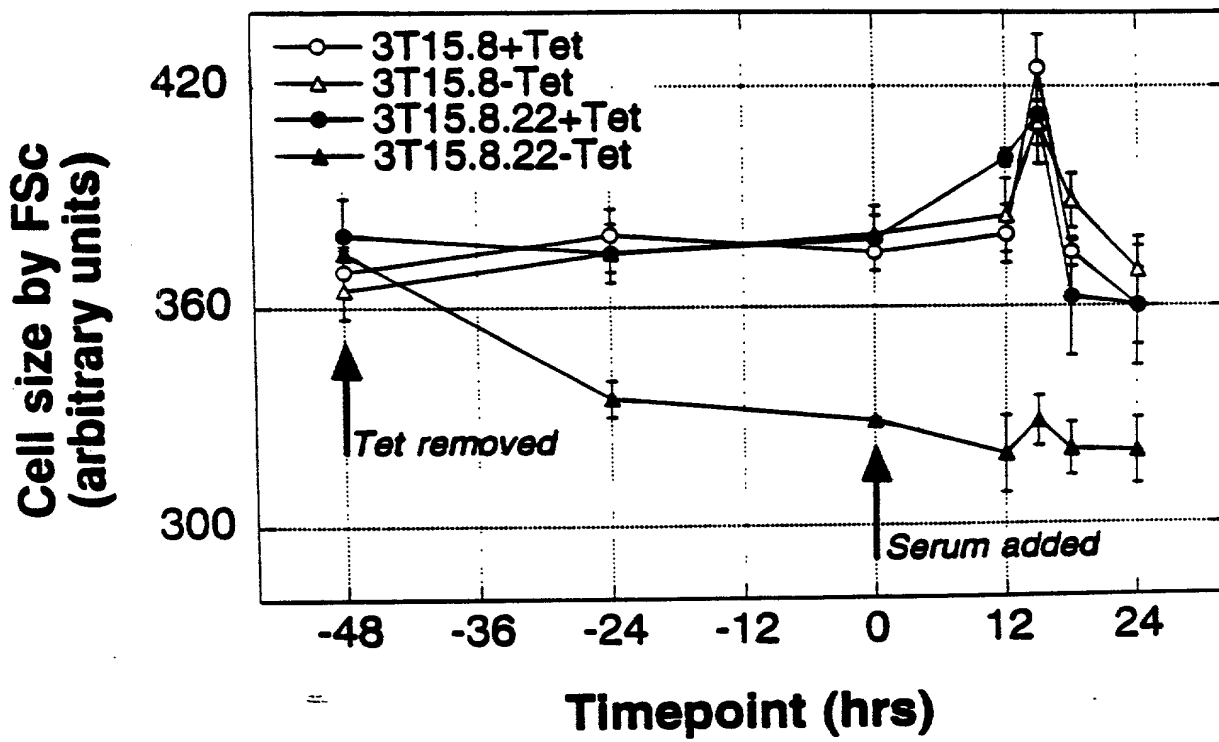


Fig. 9

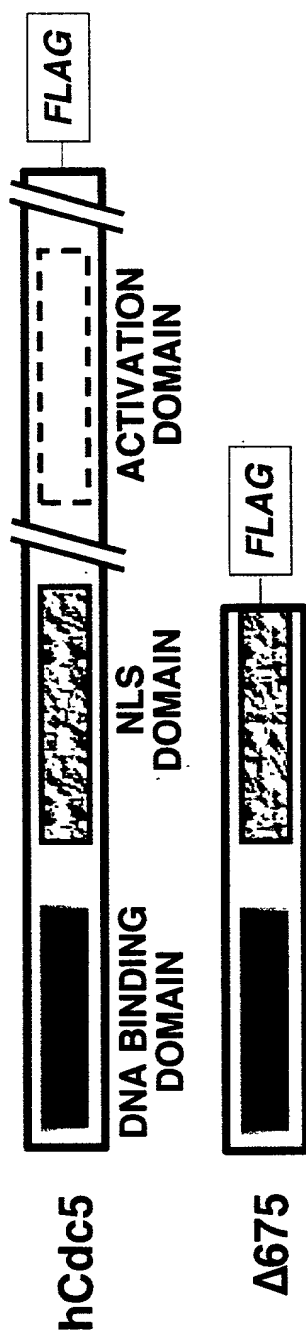


Fig. 10

708070-64025260

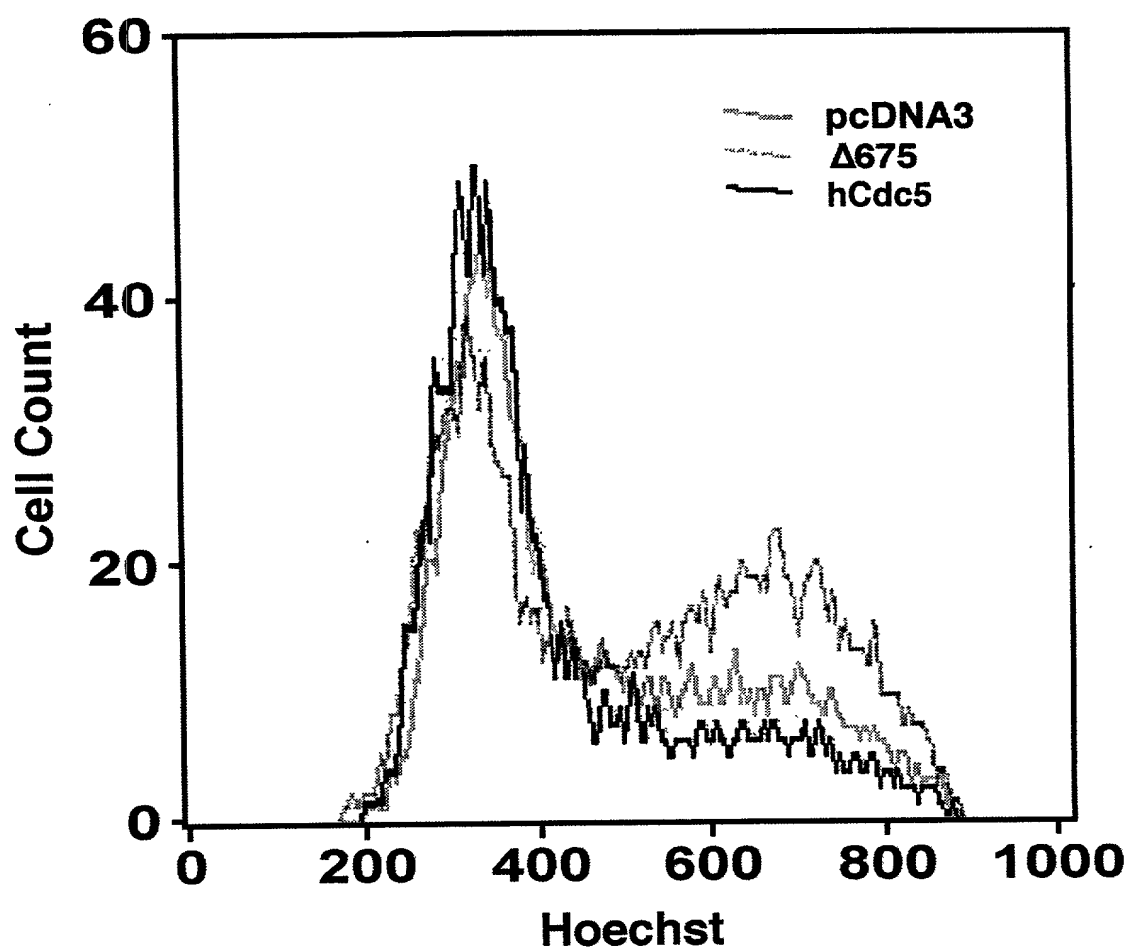


FIG. 11

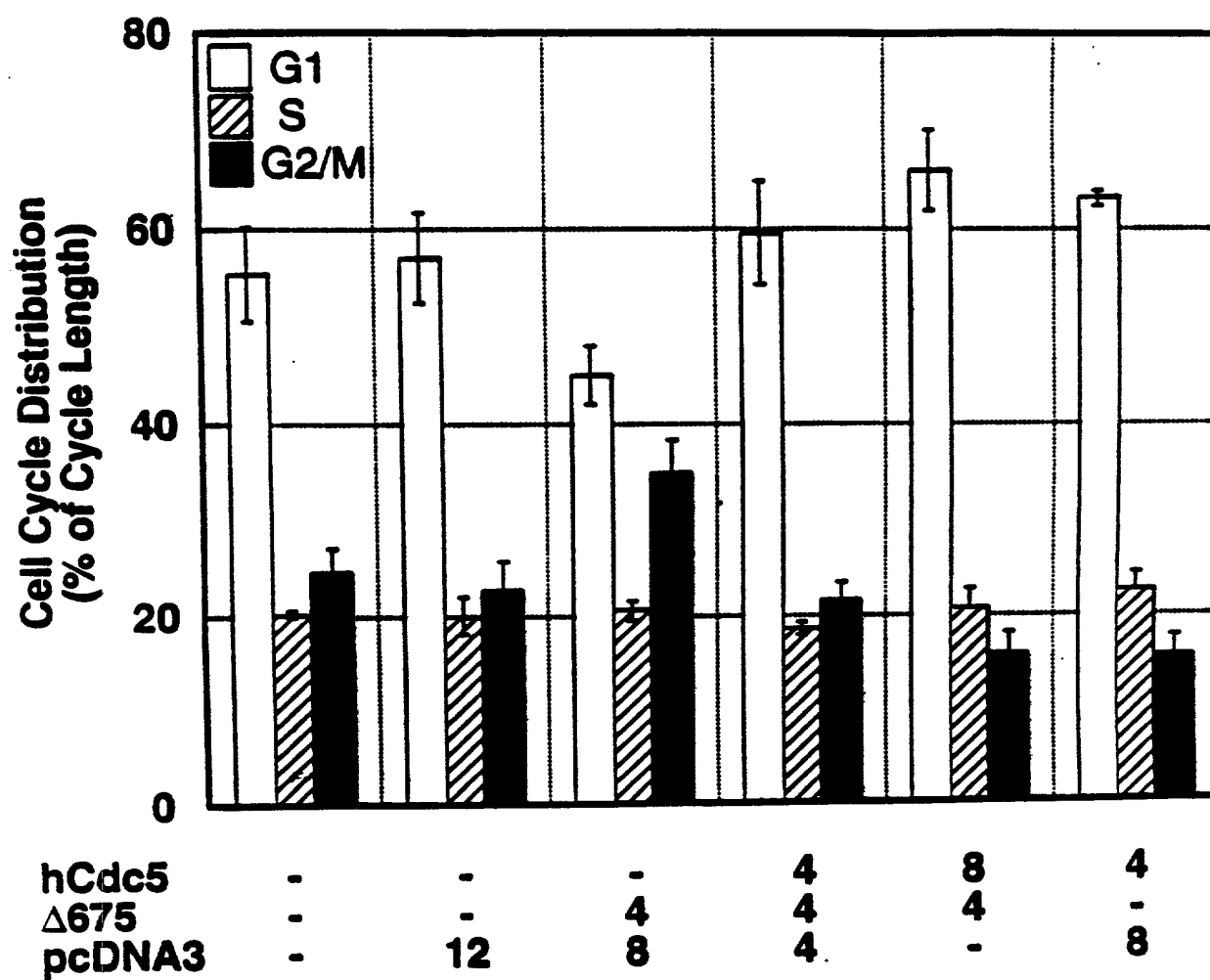


Fig. 12

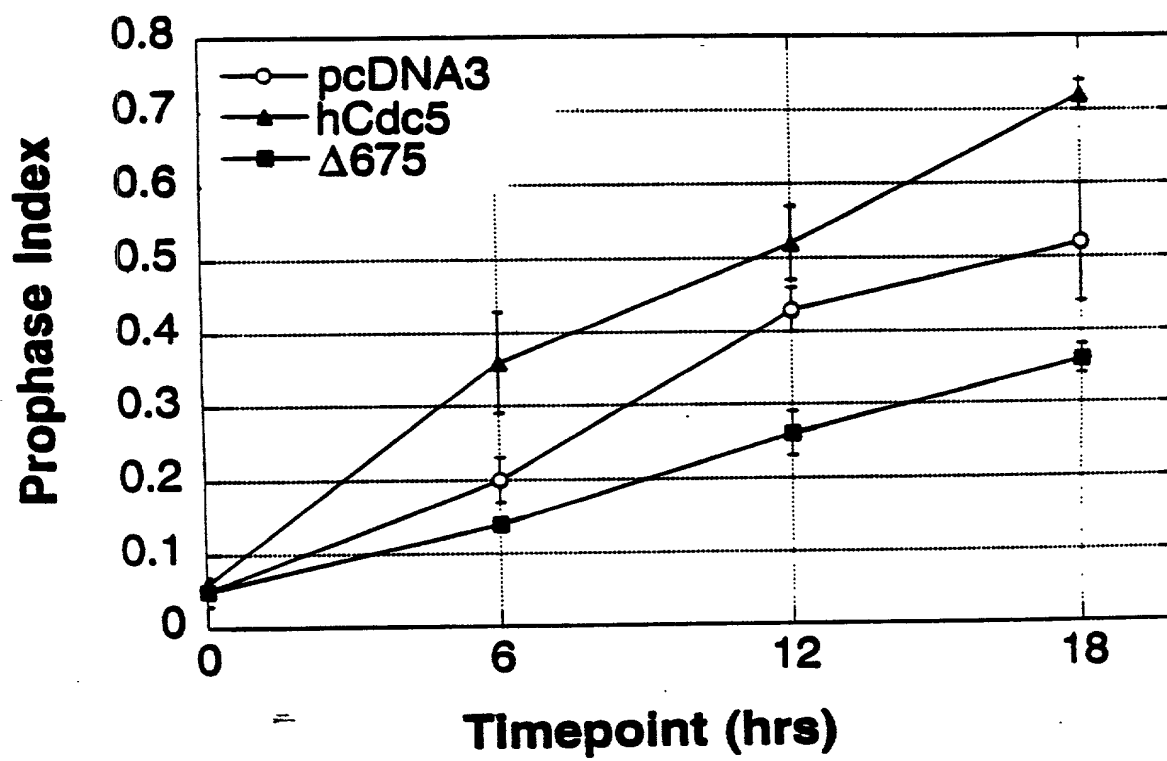
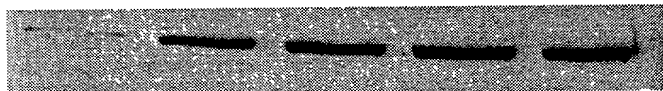
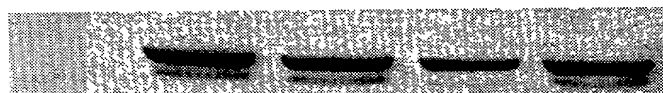


Fig. 13

0 12 15 18 21 hrs



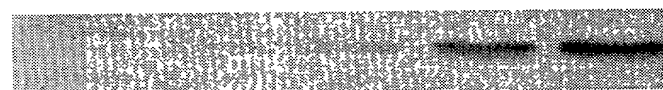
hCdc5



p50 CLNE



p60 CLNA



p62 CLNB1

FIG. 14A

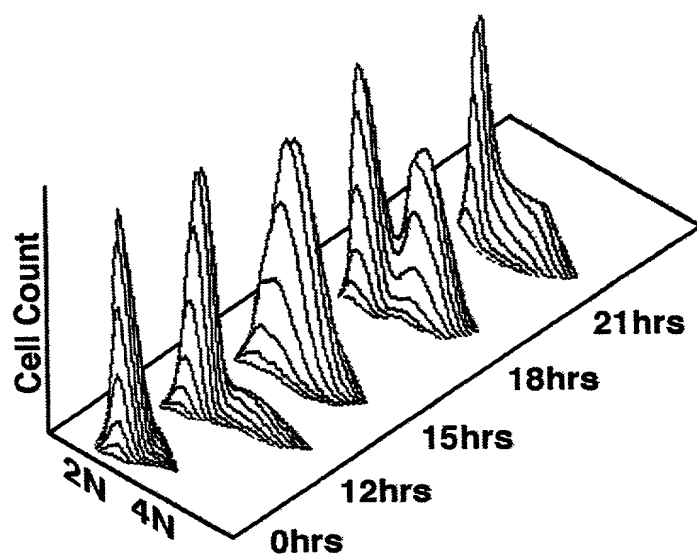


FIG. 14B

Consensus	G A T T T A A C A T A A	(SEQ ID NO:13)
8.05	G A T T T A A C A T A A	
8.04	G A T T T A A C A T A A	
8.03	G A T T T A A C A T A A	
8.02	G A T T T A A C A T A A	
8.01	G A T T T A A C A T A A	
6.05	G G T G T A A C G T G G	(SEQ ID NO:36)
6.04	G T G T T A C C A C A T	(SEQ ID NO:37)
6.03	C C A T A A A T T T A G	(SEQ ID NO:38)
6.02	G A G A T A A A G T C T	(SEQ ID NO:39)
6.01	G T G T T A T T G A A A	(SEQ ID NO:40)
3.05	A C C C A C G T C T A T	(SEQ ID NO:41)
3.04	G G T T A G G A T A G G	(SEQ ID NO:42)
3.03	G T T G A G T A G T A T	(SEQ ID NO:43)
3.02	C T G T T A A T T T C C	(SEQ ID NO:44)
3.01	G G T G T T A T T G A T	(SEQ ID NO:45)

FIG 15